GEPHE SUMMARY

Gephebase Gene

Dopamine N-acetyltransferase (Dat) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Dopamine N-acetyltransferase (Dat)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000234

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait

Coloration (puparium) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (puparium)^#gephebase-summary-title)

Trait State in Taxon A

Drosophila americana

Trait State in Taxon B

Drosophila virilis

Ancestral State

Taxon A

Taxonomic Status

Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name

Drosophila americana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila americana^#gephebase-summary-title)

Common Name

-

Synonyms

-

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Drosophila; virilis group

Parent

virilis group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32335)

NCBI Taxonomy ID

40366 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 40366)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Drosophila virilis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila virilis^#gephebase-summary-title)

Common Name

-

Synonyms

Drosophila virilis Sturtevant, 1916; Drosophila irilis

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Drosophila; virilis group

Parent

virilis group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32335)

NCBI Taxonomy ID

7244 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7244)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

AANAT1

Synonyms

AANAT; AA-NAT1; aaNat; aaNAT; aaNAT1; Aanat1; AANATA; AANATB; CG3318; DAT; Dat1; Dmel\CG3318; NAT1; Dat

String

7227.FBpp0089101 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0089101)

Sequence Similarities

-

GO - Molecular Function

GO:0004059 : aralkylamine N-acetyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004059)
GO:0004060 : arylamine N-acetyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004060)

UniProtKB Drosophila melanogaster

Q94521 (http://www.uniprot.org/uniprot/Q94521)

GenebankID or UniProtKB

()

GO:0008080 : N-acetyltransferase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0008080)

GO - Biological Process

GO:0042420 : dopamine catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042420)
GO:0006584 : catecholamine metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006584)
GO:0048066 : developmental pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048066)
GO:0030187 : melatonin biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0030187)
GO:0046334 : octopamine catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0046334)
GO:0045187 : regulation of circadian sleep/wake cycle, sleep
(https://www.ebi.ac.uk/QuickGO/term/GO:0045187)
GO:0042429 : serotonin catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042429)
GO:0030431 : sleep (https://www.ebi.ac.uk/QuickGO/term/GO:0030431)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)

Molecular Type

Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title)

Aberration Type

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)

Molecular Details of the Mutation

Not identified ; 11kb mapped interval including regulatory region and first exon

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

Main Reference

A single gene causes an interspecific difference in pigmentation in Drosophila. (2015) (https://pubmed.ncbi.nlm.nih.gov/25769982)

Authors

Ahmed-Braimah YH; Sweigart AL

Abstract

The genetic basis of species differences remains understudied. Studies in insects have contributed significantly to our understanding of morphological evolution. Pigmentation traits in particular have received a great deal of attention and several genes in the insect pigmentation pathway have been implicated in inter- and intraspecific differences. Nonetheless, much remains unknown about many of the genes in this pathway and their potential role in understudied taxa. Here we genetically analyze the puparium color difference between members of the virilis group of Drosophila. The puparium of Drosophila virilis is black, while those of D. americana, D. novamexicana, and D. lummei are brown. We used a series of backcross hybrid populations between D. americana and D. virilis to map the genomic interval responsible for the difference between this species pair. First, we show that the pupal case color difference is caused by a single Mendelizing factor, which we ultimately map to an â^¼11-kb region on chromosome 5. The mapped interval includes only the first exon and regulatory region(s) of the dopamine N-acetyltransferase gene (Dat). This gene encodes an enzyme that is known to play a part in the insect pigmentation pathway. Second, we show that this gene is highly expressed at the onset of pupation in light brown taxa (D. americana and D. novamexicana) relative to D. virilis, but not in the dark brown D. lummei. Finally, we examine the role of Dat in adult pigmentation between D. americana (heavily melanized) and D. novamexicana (lightly melanized) and find no discernible effect of this gene in adults. Our results demonstrate that a single gene is entirely or almost entirely responsible for a morphological difference between species.

Additional References

RELATED GEPHE

Related Genes

3 (Dat, ebony, tan) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^40366^/and+Trait=Coloration/or+Taxon ID=^7244^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS